//3/ #8 OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/044,477

DATE: 02/06/2002
TIME: 16:19:38

Input Set : N:\Crf3\RULE60\10044477.raw
Output Set: N:\CRF3\02062002\J044477.raw

SEQUENCE LISTING

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 1 (1) GENERAL INFORMATION:
 2        (i) APPLICANT: Hillman, Jennifer L.
 3                       Corley, Neil C.
 4                       Shah, Purvi
 5      (ii) TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
 6     (iii) NUMBER OF SEQUENCES: 3
 7      (iv) CORRESPONDENCE ADDRESS:
 8            (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 9            (B) STREET: 3174 Porter Drive
10            (C) CITY: Palo Alto
11            (D) STATE: CA
12            (E) COUNTRY: USA
13            (F) ZIP: 94304
14       (v) COMPUTER READABLE FORM:
15            (A) MEDIUM TYPE: Diskette
16            (B) COMPUTER: IBM Compatible
17            (C) OPERATING SYSTEM: DOS
18            (D) SOFTWARE: FastSEQ for Windows Version 2.0
20      (vi) CURRENT APPLICATION DATA:
C--> 21            (A) APPLICATION NUMBER: US/10/044,477
C--> 22            (B) FILING DATE: 10-Jan-2002
24     (vii) PRIOR APPLICATION DATA:
26            (A) APPLICATION NUMBER: US/09/365,705
27            (B) FILING DATE: 02-Aug-1999
30            (A) APPLICATION NUMBER: US/08/950,168
31            (B) FILING DATE: 14-OCT-1997
33    (viii) ATTORNEY/AGENT INFORMATION:
34            (A) NAME: Billings, Lucy J.
35            (B) REGISTRATION NUMBER: 36,749
36            (C) REFERENCE/DOCKET NUMBER: PF-0401 US
37      (ix) TELECOMMUNICATION INFORMATION:
38            (A) TELEPHONE: 650-855-0555
39            (B) TELEFAX: 650-845-4166
40            (C) TELEX:
41 (2) INFORMATION FOR SEQ ID NO: 1:
42        (i) SEQUENCE CHARACTERISTICS:
43            (A) LENGTH: 144 amino acids
44            (B) TYPE: amino acid
45            (C) STRANDEDNESS: single
46            (D) TOPOLOGY: linear
47      (vii) IMMEDIATE SOURCE:
48            (A) LIBRARY: BLADNOT04
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ENTERED

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          ·   PATENT APPLICATION:  US/10/044,477   TIME: 16:19:38

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49              (B) CLONE: 1318847
50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51        Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu
52         1               5               10              15
53        Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
54                    20              25              30
55        Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu
56             35              40              45
57        Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val
58             50              55              60
59        Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro
60        65              70              75              80
61        Leu Leu Ala Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser
62                    85              90              95
63        Gly Pro Gly Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu
64                 100             105             110
65        Ala Tyr Cys Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu
66             115             120             125
67        Ala Phe Phe Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
68             130             135             140
70  (2) INFORMATION FOR SEQ ID NO: 2:
71      (i) SEQUENCE CHARACTERISTICS:
72          (A) LENGTH: 1391 base pairs
73          (B) TYPE: nucleic acid
74          (C) STRANDEDNESS: single
75          (D) TOPOLOGY: linear
76   (vii) IMMEDIATE SOURCE:
77          (A) LIBRARY: BLADNOT04
78          (B) CLONE: 1318847
79    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80        GTTTTACCCA GAGGGCCCTG CGACGCCTTT CTCCGCTGGC AACGGCGCCG CTCCCCGCTC      60
81        CTCCTCCCCA GCCATGGCGT TCACGTTCGC GGCCTTCTGC TACATGCTGG CGCTGCTGCT     120
82        CACTGCCGCG CTCATCTTCT TCGCCATTTG GCACATTATA GCATTTGATG AGCTGAAGAC     180
83        TGATTACAAG AATCCTATAG ACCAGTGTAA TACCCTGAAT CCCCTTGTAC TCCCAGAGTA     240
84        CCTCATCCAC GCTTTCTTCT GTGTCATGTT TCTTTGTGCA GCAGAGTGGC TTACACTGGG     300
85        TCTCAATATG CCCCTCTTGG CATATCATAT TTGGAGGTAT ATGAGTAGAC CAGTGATGAG    .360
86        TGGCCCAGGA CTCTATGACC CTACAACCAT CATGAATGCA GATATTCTAG CATATTGTCA     420
87        GAAGGAAGGA TGGTGCAAAT TAGCTTTTTA TCTTCTAGCA TTTTTTTACT ACCTATATGG     480
88        CATGATCTAT GTTTTGGTGA GCTCTTAGAA CAACACACAG AAGAATTGGT CCAGTTAAGT     540
89        GCATGCAAAA AGCCACCAAA TGAAGGGATT CTATCCAGCA AGATCCTGTC CAAGAGTAGC     600
90        CTGTGGAATC TGATCAGTTA CTTTAAAAAA TGACTCCTTA TTTTTTAAAT GTTTCCACAT     660
91        TTTTGCTTGT GGAAAGACTG TTTTCATATG TTATACTCAG ATAAAGATTT TAAATGGTAT     720
92        TACGTATAAA TTAATATAAA ATGATTACCT CTGGTGTTGA CAGGTTTGAA CTTGCACTTC     780
93        TTAAGGAACA GCCATAATCC TCTGAATGAT GCATTAATTA CTGACTGTCC TAGTACATTG     840
94        GAAGCTTTTG TTTATAGGAA CTTGTAGGGC TCATTTTGGT TTCATTGAAA CAGTATCTAA     900
95        TTATAAATTA GCTGTAGATA TCAGGTGCTT CTGATGAAGT GAAAATGTAT ATCTGACTAG     960
96        TGGGAAACTT CATGGGTTTC CTCATCTGTC ATGTCGATGA TTATATATGG ATACATTTAC    1020
97        AAAAATAAAA AGCGGGAATT TTCCCTTCGC TTGAATATTA TCCCTGTATA TTGCATGAAT    1080
98        GAGAGATTTC CCATATTTCC ATCAGAGTAA TAAATATACT TGCTTTAATT CTTAAGCATA    1140
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 99      AGTAAACATG ATATAAAAAT ATATGCTGAA TTACTTGTGA AGAATGCATT TAAAGCTATT    1200
100      TTAAATGTGT TTTTATTTGT AAGACATTAC TTATTAAGAA ATTGGTTATT ATGCTTACTG    1260
101      TTCTAATCTG GTGGTAAAGG TATTCTTAAG AATTTGCAGG TACTACAGAT TTTCAAAACT    1320
102      GAATGAGAGA AAATTGTATA ACCATCCTGC TGTTCCTTTA GTGCAATACA ATAAAACTCT    1380
103      GAAATTAAAA A                                                         1391
105 (2) INFORMATION FOR SEQ ID NO: 3:
106      (i) SEQUENCE CHARACTERISTICS:
107          (A) LENGTH: 144 amino acids
108          (B) TYPE: amino acid
109          (C) STRANDEDNESS: single
110          (D) TOPOLOGY: linear
111     (vii) IMMEDIATE SOURCE:
112          (A) LIBRARY: GenBank
113          (B) CLONE: 886769
114     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
115      Met Ala Phe Asn Phe Thr Ala Phe Thr Tyr Ile Val Ala Leu Ile Gly
116       1               5                  10                  15
117      Asp Ala Phe Leu Ile Phe Phe Ala Ile Phe His Val Ile Ala Phe Asp
118              20                  25                  30
119      Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Ser Leu
120              35                  40                  45
121      Asn Pro Leu Val Leu Pro Glu Tyr Leu Leu His Ile Phe Leu Asn Leu
122          50                  55                  60
123      Leu Phe Leu Phe Cys Gly Glu Trp Phe Ser Leu Cys Ile Asn Ile Pro
124      65                  70                  75                  80
125      Leu Ile Ala Tyr His Ile Trp Arg Tyr Lys Asn Arg Pro Val Met Ser
126                  85                  90                  95
127      Gly Pro Gly Leu Tyr Asp Pro Thr Thr Val Leu Lys Thr Asp Thr Leu
128                  100                 105                 110
129      Tyr Arg Asn Met Arg Glu Gly Trp Ile Lys Leu Ala Val Tyr Leu Ile
130                  115                 120                 125
131      Ser Phe Phe Tyr Tyr Ile Tyr Gly Met Val Tyr Ser Leu Ile Ser Thr
132                  130                 135                 140
```

VERIFICATION SUMMARY   DATE: 02/06/2002
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L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]